

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 27, 2005, 04:35:15 ; Search time 1960 Seconds
(without alignments)
580.035 Million cell updates/sec

Title: US-10-605-498-82

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Total number of hits satisfying chosen parameters: 1681110

Minimum DB seq length: 12
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	19	95.0	19	6	CQ799992 Sequence
4	16	80.0	21	6	CQ799905 Sequence
5	15	75.0	21	6	CQ799906 Sequence
6	14.2	71.0	33	6	AR559501 Sequence
7	14.2	71.0	33	6	AX473165 Sequence
8	13.2	66.0	27	6	E41696 Process for
9	13	65.0	20	6	AR454276 Sequence
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11	12.8	64.0	23	6	AX034952 Sequence
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15	12.6	63.0	24	6	AR579704 Sequence
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17	12.6	63.0	30	6	AR229807 Sequence
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19	12.4	62.0	20	6	AR014592 Sequence
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34	12.2	61.0	22	6	AR374615 Sequence
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36	12.2	61.0	22	6	AX430044 Sequence
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ALIGNMENTS

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LOCUS CQ799984 20 bp DNA linear PAT 28-APR-2004
DEFINITION Sequence 82 from Patent WO2004030660.
ACCESSION CQ799984
VERSION CQ799984.1 GI:46848931

KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens

REFERENCE 1
AUTHORS Gleave, M.E., Rocchi, P. and Signaevsky, M.
TITLE Compositions for treatment of prostate and other cancers
JOURNAL Patent: WO 2004030660-A 82 15-APR-2004;
The University of British Columbia (CA)

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DEFINITION Sequence 81 from Patent WO2004030660.
ACCESSION CQ799983
VERSION CQ799983.1 GI:46848930
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.

REFERENCE 1
AUTHORS Gleave, M.E., Rocchi, P. and Signaevsky, M.
TITLE Compositions for treatment of prostate and other cancers
JOURNAL Patent: WO 2004030660-A 81 15-APR-2004;
The University of British Columbia (CA)
LOCATION/Qualifiers

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ACCESSION CQ799992
VERSION CQ799992.1 GI:46848939
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.

REFERENCE 1
AUTHORS Gleave, M.E., Rocchi, P. and Signaevsky, M.
TITLE Compositions for treatment of prostate and other cancers
JOURNAL Patent: WO 2004030660-A 90 15-APR-2004;
The University of British Columbia (CA)
LOCATION/Qualifiers

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Qy 2 GGACGGCGCTCGGTTCAT 20
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Db 19 GGACGGCGCTCGGTTCAT 1

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LOCUS CQ799905 21 bp DNA linear PAT 28-APR-2004
DEFINITION Sequence 3 from Patent WO2004030660.
ACCESSION CQ799905
VERSION CQ799905.1 GI:46848852
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.

REFERENCE 1
AUTHORS Gleave, M.E., Rocchi, P. and Signaevsky, M.
TITLE Compositions for treatment of prostate and other cancers

JOURNAL Patent: WO 2004030660-A 3 15-APR-2004;
The University of British Columbia (CA)
LOCATION/Qualifiers

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Db 1 CGCGCGCTCGGTTCAT 16

RESULT 5
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DEFINITION Sequence 4 from Patent WO2004030660.
ACCESSION CQ799906
VERSION CQ799906.1 GI:46848853
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.

REFERENCE 1
AUTHORS Gleave, M.E., Rocchi, P. and Signaevsky, M.
TITLE Compositions for treatment of prostate and other cancers
JOURNAL Patent: WO 2004030660-A 4 15-APR-2004;
The University of British Columbia (CA)
LOCATION/Qualifiers

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/db_xref="taxon:9606"

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Db 7 GGGACGGCGCTCG 21

RESULT 6
LOCUS AR559501 33 bp DNA linear PAT 08-OCT-2004
DEFINITION Sequence 16 from patent US 6750042.
ACCESSION AR559501
VERSION AR559501.1 GI:53968947
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 33)
AUTHORS Summers, A.O. and Cagliati, J.J.
TITLE Metal binding proteins, recombinant host cells and methods
JOURNAL Patent: US 6750042-A 16 15-JUN-2004;
University of Georgia Research Foundation, Inc.; Athens, GA
LOCATION/Qualifiers

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/mol_type="genomic DNA"

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Db 6 GGGTCTCGGCGCTCGGCA 24

RESULT 7
AX473165
LOCUS AX473165 33 bp DNA linear PAT 09-AUG-2002
DEFINITION Sequence 16 from Patent WO230962.
ACCESSION AX473165
VERSION AX473165.1 GI:22207875
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.

REFERENCE 1
AUTHORS Summers,A.O. and Caguiat,J.J.
TITLE Metal binding proteins, recombinant host cells and methods
JOURNAL Patent: WO 0230962-A 16 18-APR-2002;
UNIVERSITY OF GEORGIA RESEARCH FOUNDATION, INC. (US)

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/db_xref="taxon:32630"
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QY 1 GGGACGGCGCTCGGTCA 19
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Db 6 GGGTCTCGGCGCTCGGCA 24

RESULT 8
E41696
LOCUS E41696 27 bp DNA linear PAT 31-JAN-2002
DEFINITION Process for producing L-glutamic acid by fermentation.
ACCESSION E41696
VERSION E41696.1 GI:18633367
KEYWORDS JP 2001069979-A/13.
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.

REFERENCE 1 (bases 1 to 27)
AUTHORS Fujii,M. and Imanaka,T.
TITLE Process for producing L-glutamic acid by fermentation
JOURNAL Patent: JP 2001069979-A 13 21-MAR-2001;
JAPAN TOBACCO INC,TAKAYUKI IMANAKA

COMMENT OS Artificial Sequence
PN JP 2001069979-A/13
PD 21-MAR-2001
PF 31-AUG-1999 JP 1999245121

PI MIKIO FUJII, TADAYUKI IMANAKA
PC C12N15/09,C12N1/21,C12P13/14/(C12N1/21,C12R1:15),(C12P13/14,
PC C12R1:15),
PC C12N15/00

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source 1. .27
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QY 3 GACGCGCGCTCGGTCA 20
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Db 9 GACGCGCGACGCCCAT 26

RESULT 9
AR454276
LOCUS AR454276 20 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 19 from patent US 6680425.
ACCESSION AR454276
VERSION AR454276.1 GI:42687423
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 20)
AUTHORS Rodriguez,R.L.
TITLE Chimeric plant promoters comprising sugar-regulatory sequences
JOURNAL Patent: US 6680425-A 19 20-JAN-2004;
The Regents of the University of California; Oakland, CA

FEATURES
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/organism="unknown"
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QY 3 GACGCGCGCTCG 15
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Db 2 GACGCGCGCTCG 14

RESULT 10
BD243529
LOCUS BD243529/c 23 bp DNA linear PAT 17-JUL-2003
DEFINITION Nucleotide fragment, probe, primer, reagent, and method for detecting nucleotide sequence derived from replication origin of pBR322.

ACCESSION BD243529
VERSION BD243529.1 GI:33053299
KEYWORDS JP 2002537856-A/36.
SOURCE unidentified
ORGANISM unidentified.

REFERENCE 1 (bases 1 to 23)
AUTHORS Lamy,D.
TITLE Nucleotide fragment, probe, primer, reagent, and method for detecting nucleotide sequence derived from replication origin of pBR322.
JOURNAL Patent: JP 2002537856-A 36 12-NOV-2002;
TRANSGENE

COMMENT OS pBR322 plasmid
PN JP 2002537856-A/36
PD 12-NOV-2002
PF 03-MAR-2000 JP 2000603424
PR 05-MAR-1999 FR 99/02968
PI DIDIER LAMY
PC C12N15/09,C12Q1/68,C12N15/00
CC Nucleotide fragment, probe, primer, reagent, and method for detecting
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Qy 5 CGCGCGCTCGGTCAT 20
Db 16 CGTGCCTCGGTCGT 1

RESULT 11
AX034952/c
LOCUS AX034952 23 bp DNA linear PAT 15-NOV-2000
DEFINITION Sequence 36 from Patent WO0053803.
ACCESSION AX034952
VERSION AX034952.1 GI:11190877
KEYWORDS Cloning vector pBR322
SOURCE Cloning vector pBR322
ORGANISM Cloning vector pBR322
REFERENCE 1
AUTHORS Lamy D.
TITLE Nucleotide fragment, probe, primer, reagent and method for
detecting a nucleotide sequence derived from pBR322 replication
origin
JOURNAL Patent: WO 0053803-A 36 14-SEP-2000;
LAMY DIDIER (FR); TRANSGENE (FR)
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Qy 5 CGCGCGCTCGGTCAT 20
Db 16 CGTGCCTCGGTCGT 1

RESULT 12
AX684030
LOCUS AX684030 24 bp DNA linear PAT 29-MAR-2003
DEFINITION Sequence 3 from Patent WO03006502.
ACCESSION AX684030
VERSION AX684030.1 GI:29371014
KEYWORDS Danio rerio (zebrafish)
SOURCE Danio rerio
ORGANISM Danio rerio
REFERENCE 1
AUTHORS Langheinrich U.
TITLE Isolation, characterization, and use of a teleost potassium channel
JOURNAL Patent: WO 03006502-A 3 23-JAN-2003;
Exelixis Deutschland GmbH (DE)
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/organism="Danio rerio"
/mol_type="unassigned DNA"
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Qy 5 CGCGCGCTCGGTCAT 20
Db 16 CGTGCCTCGGTCGT 1

RESULT 13
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LOCUS BD081436 24 bp DNA linear PAT 27-AUG-2002
DEFINITION Production of proteins in plant seeds.
ACCESSION BD081436
VERSION BD081436.1 GI:22627039
KEYWORDS JP 2001518305-A/10.
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 24)
AUTHORS Lemaux P.G., Cho M.J. and Buchanan R.B.
TITLE Production of proteins in plant seeds
JOURNAL Patent: JP 2001518305-A 10 16-OCT-2001;
THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
COMMENT OS Artificial Sequence
PN JP 2001518305-A/10
PD 16-OCT-2001
PF 30-SEP-1998 JP 2000513959
PR 30-SEP-1997 US 60/060510
PI PEGGY G LEMAUX, MYEONG JE CHO, ROBERT B BUCHANAN PC
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Db 19 GCACGAGCGCTCGGATAT 1

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AR429358/c
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DEFINITION Sequence 12 from patent US 6642437.
ACCESSION AR429358
VERSION AR429358.1 GI:40189549
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 24)
AUTHORS Lemaux P.G., Cho M.-J. and Buchanan R.B.
TITLE Production of proteins in plant seeds
JOURNAL Patent: US 6642437-A 12 04-NOV-2003;
The Regents of the University of California; Oakland, CA
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Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 GGACGGCGCGCTCGGTCAT 20
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Db 19 GCACGAGCGCTCGGATAT 1

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AR579704/c
LOCUS AR579704 24 bp DNA linear PAT 14-DEC-2004
DEFINITION Sequence 14 from patent US 6784346.
ACCESSION AR579704
VERSION AR579704.1 GI:56583159

KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 24)
AUTHORS Cho, M.-J., Lemaux, P.G., Buchanan, B.B., Wong, J. and Marx, C.
TITLE Value-added traits in grain and seed transformed with thioredoxin
JOURNAL Patent: US 6784346-A 14 31-AUG-2004;
The Regents of the University of California; Oakland, CA

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Search completed: November 27, 2005, 05:29:43
Job time : 1963 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 27, 2005, 03:35:40 ; Search time 478 Seconds
(without alignments)
278.857 Million cell updates/sec

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Perfect score: 20
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Gapop 10.0 , Gapext 1.0

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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C 32	12.4	62.0	20	2 AAV35805	Aav35805 PCR prime
C 33	12.4	62.0	20	2 AAV99501	Aav99501 Plasmid p
C 34	12.4	62.0	20	8 ADA16031	Ada16031 Plasmid p
C 35	12.4	62.0	20	9 ACH03677	Ach03677 Plasmid p
C 36	12.4	62.0	20	10 ADF73001	Adf73001 Probe rel
C 37	12.4	62.0	20	14 ADW71639	Adw71639 Plasmid p
C 38	12.4	62.0	24	6 ABQ07627	Abq07627 Oligonucl
C 39	12.4	62.0	24	6 ABQ01856	Abq01856 Oligonucl
C 40	12.4	62.0	24	6 ABQ07668	Abq07668 Oligonucl
C 41	12.4	62.0	24	12 ADO38198	Ado38198 HIV envel
C 42	12.4	62.0	24	12 ADO38213	Ado38213 HIV envel
C 43	12.4	62.0	24	12 ADO38185	Ado38185 HIV envel
C 44	12.4	62.0	24	12 ADO38102	Ado38102 HIV envel
C 45	12.4	62.0	24	12 ADO38074	Ado38074 HIV envel

ALIGNMENTS

RESULT 1
ADM94732
ID ADM94732 standard; DNA; 20 BP.

AC ADM94732;
XX
DT 01-JUL-2004 (first entry)

XX Human heat shock protein 27 antisense oligonucleotide SEQ ID NO:82.
DE heat shock protein 27; hsp27; cytostatic; gene therapy;
KW heat shock protein 27 inhibitor; hsp27 inhibitor; cancer; human;
KW antisense oligonucleotide; ss.

XX Homo sapiens.
OS Synthetic.

XX WO2004030660-A2.

PN 15-APR-2004.

XX 02-OCT-2003; 2003WO-CA001588.

XX 02-OCT-2002; 2002US-0415859P.

PR 18-APR-2003; 2003US-0463952P.

XX (UYBR-) UNIV BRITISH COLUMBIA.

PI Gleave MB, Rocchi P, Signaevsky M;

XX WPI; 2004-316331/29.

XX New composition comprising a therapeutic agent that reduces the amount of
PT active hsp27 in hsp27 expressing cells exposed to the therapeutic agent,
PT useful in treating cancer, e.g., prostate cancer or a central nervous
PT system malignancy.

XX Claim 6; SEQ ID NO 82; 38pp; English.

XX The present invention describes a composition which comprises a
CC therapeutic agent that reduces the amount of active heat shock protein 27
CC (hsp27) in hsp27 expressing cells exposed to the therapeutic agent. The

PT soil, water, aqueous medium including biological fluids.
XX Disclosure; Page 24; 42pp; English.
XX
CC The present invention relates to a new non-naturally occurring
CC recombinant DNA molecule comprising a sequence encoding a chelon protein
CC which binds mercuric ions. The invention is useful for recombinantly
CC producing a protein in a host-cell, by infecting or transforming a host
CC cell capable of expressing a chelon coding sequence with a vector
CC comprising a promoter active in the host cell operably linked to a coding
CC region for the protein to produce a recombinant host cell and culturing
CC the recombinant host cell under conditions, where DNA is expressed. The
CC nucleic acid encoding the chelon protein is useful for binding divalent
CC mercuric ions, to take up, sequester and concentrate the heavy metal ions
CC from contaminated soil, ground water, hydroponic solutions or irrigation
CC water of waste streams. The DNA of the invention, when immobilised onto a
CC solid support, is useful for concentrating heavy metal ions from
CC contaminated environment waste streams or contaminated aqueous medium
CC including biological fluids. The nucleic acid, when recombinantly
CC expressed in enteric bacteria (which are nontoxic and nonpathogenic),
CC is suitable for use in the in vivo sequestration and elimination of
CC mercuric ion from gastrointestinal tracts of animals or humans exposed to
CC toxic metal ions such as mercury and/or cadmium. The molecules of the
CC invention are also useful in water treatment resins. The nucleic acid of
CC the invention is highly specific and binds divalent cation such as
CC mercury or cadmium with high affinity. The present nucleic acid sequence
CC represents synthetic product 2 reverse PCR primer that was used in the
CC methods of the invention for construction of pASK-MBD vector
XX
SQ Sequence 33 BP; 6 A; 8 C; 12 G; 7 T; 0 U; 0 Other;

Query Match 71.0%; Score 14.2; DB 6; Length 33;
Best Local Similarity 84.2%; Pred. No. 5.4e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GGACGGCGCGCTCGGTCA 19
||| ||||| |||
Db 6 GGGTCTCGCGCTCGGCA 24

RESULT 7
ACH58106
ID ACH58106 standard; DNA; 25 BP.

XX ACH58106;

DT 16-OCT-2003 (first entry)

DE DNA target sequence #7242 useful in array for genetic analyses.

XX Gene expression analysis; array; hybridisation; genetic variation;
KW tag-labelled compound; gene family; in situ hybridisation;
KW library screening; Southern hybridisation; northern hybridisation;
KW dot-blot hybridisation; gene sequence; mutation detection;
KW target sequence; probe; PCR; primer; ss.

XX Unidentified.

XX US2003082596-A1.

XX 01-MAY-2003.

XX 08-AUG-2002; 2002US-00215112.

XX 08-AUG-2001; 2001US-0311040P.

XX (MITT/) MITTMANN M.

XX Mittmann M;

XX WPI; 2003-576608/54.

PT New probe array useful e.g. for monitoring gene expression levels, for

PT analyzing genetic variations, or for hybridizing tag-labeled compounds,
PT comprises multiple nucleic acid probes.
XX
PS Claim 1; SEQ ID NO 7242; 9pp; English.

XX
CC The present invention relates to nucleic acid sequences that are
CC complementary to particular genes, and can be used as probes for a
CC variety of analyses such as gene expression analysis. Each probe
CC comprises 9 or more consecutive nucleotides from at least one of 14936
CC nucleotide sequences defined in the patent, or their perfect sense match,
CC sense mismatch, antisense match or antisense mismatch oligonucleotides.
CC The probes may be used in an array comprising at least 10 distinct
CC nucleic acid probes. The array is useful in monitoring gene expression
CC levels by hybridisation to a DNA library, in analysing genetic
CC variations, and in hybridising tag-labelled compounds. The probes are
CC useful for identifying family members of a gene. The probes are also
CC useful in situ hybridisations, in screening cDNA or genomic libraries
CC (or derived subclones) for additional clones containing segments of DNA
CC that have been previously isolated and sequenced, in Southern, northern,
CC or dot-blot hybridisation of genomic DNA to identify or detect the
CC sequence of any gene or detect specific mutations in any gene, and in
CC mapping the 5' termini of mRNA molecules by primer extensions. The
CC nucleic acid sequences of the invention are also useful as PCR primers.
CC The invention provides a large collection of nucleic acid sequences
CC complementary to particular genes with a wide range of analytical uses.
CC ACH50865-ACH65260 represent the target sequences of the invention. Note:
CC The sequence data for this patent was obtained in electronic format
CC directly from the USPTO web site at seqdata.uspto.gov/psipdIDentry.html
XX
SQ Sequence 25 BP; 4 A; 9 C; 9 G; 3 T; 0 U; 0 Other;

Query Match 70.0%; Score 14; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 6.8e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GGACGGCGCGCTCG 15
||| ||||| |||
Db 2 GGACGGCGCGCTCG 15

RESULT 8
ACI03862/c
ID ACI03862 standard; DNA; 25 BP.

XX ACI03862;

DT 13-OCT-2003 (first entry)

DE Human microarray DNA oligonucleotide SEQ ID NO 3853.

XX EST; ss; probe; expressed sequence tag; microarray; gene expression;
KW genetic variation; diallelic marker; polymorphism; human;
KW cross-species comparison.

XX Homo sapiens.

XX US2003104410-A1.

XX 05-JUN-2003.

XX 15-MAR-2002; 2002US-00098263.

XX 16-MAR-2001; 2001US-0276759P.

XX (AFFY-) AFFYMETRIX INC.

XX Mittmann MP;

XX WPI; 2003-567953/53.

XX New array of nucleic acid probes, useful for in situ hybridization, in
PT Southern, Northern or dot-blot hybridization to identify or detect the
PT sequence or specific mutations of any gene.

XX Claim 1; SEQ ID NO 3853; 9pp; English.

XX The invention discloses a microarray comprising a plurality of nucleic acid probes including one of 2,018,500 fully defined sequences, or its perfect match, perfect mismatch, antisense match or antisense mismatch. CC Also disclosed is a method of gene expression analysis. The array is used in monitoring gene expression levels by hybridisation to a DNA library, CC in analysis of genetic variation or in hybridisation of tag-labelled compounds. The nucleic acid probes are specifically designed for analysis CC of at least one target sequence. The method of analysis comprises CC hybridising at least one or more nucleic acids to at least two or more CC nucleic acid probes and detecting the hybridisation. The nucleic acid CC probes are attached to a solid support. The analysis comprises monitoring CC gene expression levels, identifying biallelic markers or polymorphisms, CC or family members of a gene and a cross-species comparison. Each of the CC nucleic acids further comprises a tag sequence. The array of nucleic acid CC probes is useful in situ hybridisation, in Southern, Northern or dot- CC blot hybridisation to identify or detect the sequence or specific CC mutations of any gene, in mapping the 5' termini of mRNA molecules by CC primer extensions or in screening cDNA or genomic libraries or subclones CC for additional subclones containing segments of DNA that have been CC isolated and previously sequenced. The sequence presented is one of the CC nucleic acid probes incorporated in the microarray. Note: The sequence CC data for this patent can also be obtained in electronic format directly CC from USPTO at seqdata.uspto.gov/sequence.html

XX SQ Sequence 25 BP; 6 A; 8 C; 8 G; 3 T; 0 U; 0 Other;

Query Match 66.0%; Score 13.2; DB 9; Length 25;
Best Local Similarity 83.3%; Pred. No. 1.6e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GGACGGCGCGCTCGGTCA 19
||||| ||||| ||||| ||||| |||||

Db 24 GGACTCGTCGTCGTCA 7

RESULT 9

AC165798

ID AC165798 standard; DNA; 25 BP.

XX AC AC165798;

XX 14-OCT-2003 (first entry)

XX Human microarray DNA oligonucleotide SEQ ID NO 65789.

XX EST; ss; probe; expressed sequence tag; microarray; gene expression;
KW genetic variation; biallelic marker; polymorphism; human;
KW cross-species comparison.

XX Homo sapiens.

XX US2003104410-A1.

XX 05-JUN-2003.

XX 15-MAR-2002; 2002US-00098263.

XX 16-MAR-2001; 2001US-0276759P.

XX (AFFY-) AFFYMETRIX INC.

XX Mittmann MP;

XX WPI; 2003-567953/53.

XX New array of nucleic acid probes, useful for in situ hybridization, in
PT Southern, Northern or dot-blot hybridization to identify or detect the
PT sequence or specific mutations of any gene.

XX Claim 1; SEQ ID NO 65789; 9pp; English.

XX The invention discloses a microarray comprising a plurality of nucleic acid probes including one of 2,018,500 fully defined sequences, or its perfect match, perfect mismatch, antisense match or antisense mismatch. CC Also disclosed is a method of gene expression analysis. The array is used in monitoring gene expression levels by hybridisation to a DNA library, CC in analysis of genetic variation or in hybridisation of tag-labelled compounds. The nucleic acid probes are specifically designed for analysis CC of at least one target sequence. The method of analysis comprises CC hybridising at least one or more nucleic acids to at least two or more CC nucleic acid probes and detecting the hybridisation. The nucleic acid CC probes are attached to a solid support. The analysis comprises monitoring CC gene expression levels, identifying biallelic markers or polymorphisms, CC or family members of a gene and a cross-species comparison. Each of the CC nucleic acids further comprises a tag sequence. The array of nucleic acid CC probes is useful in situ hybridisation, in Southern, Northern or dot- CC blot hybridisation to identify or detect the sequence or specific CC mutations of any gene, in mapping the 5' termini of mRNA molecules by CC primer extensions or in screening cDNA or genomic libraries or subclones CC for additional subclones containing segments of DNA that have been CC isolated and previously sequenced. The sequence presented is one of the CC nucleic acid probes incorporated in the microarray. Note: The sequence CC data for this patent can also be obtained in electronic format directly CC from USPTO at seqdata.uspto.gov/sequence.html

XX SQ Sequence 25 BP; 4 A; 8 C; 9 G; 4 T; 0 U; 0 Other;

Query Match 66.0%; Score 13.2; DB 9; Length 25;
Best Local Similarity 83.3%; Pred. No. 1.6e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 GACGGCGCGCTCGGTCA 20
||||| ||||| ||||| ||||| |||||

Db 5 GACCGGAGCTCGGTCT 22

RESULT 10

AAH21740

ID AAH21740 standard; DNA; 27 BP.

XX AC AAH21740;

XX 14-AUG-2001 (first entry)

XX Corynebacterium glutamicum chaperone CpkB related PCR primer SEQ:13.

XX Corynebacterium glutamicum; chaperone; chaperonin; CpkB; groEL;
KW fermentation; L-glutamic acid; thermophilic microbe; PCR primer; ss.

XX Corynebacterium glutamicum.

XX JP2001069979-A.

XX 21-MAR-2001.

XX 31-AUG-1999; 99JP-00245121.

XX 31-AUG-1999; 99JP-00245121.

XX (NIBS) JAPAN TOBACCO INC.

XX (BEAB-) BE ABLE KK.

XX WPI; 2001-321175/34.

XX Preparation of L-glutamic acid by fermentation.

XX Example 1; Page 11; 18pp; Japanese.

XX The present invention describes an L-glutamic acid-producing microbe (I)
CC or its mutant which expresses the molecular chaperone derived from a
CC thermophilic microbe and produces stably L-glutamic acid at a temperature
CC near the upper limit of optimum growth or higher. (I) or its mutant
CC transformed by a recombinant DNA containing a gene encoding the molecular

CC chaperone derived from a thermophilic microbe and a promoter operably
CC associated with a gene (ii) comprising: (a) a fully defined 1661 base
CC pair (bp) sequence (AAH21757); (b) a nucleic acid sequence encoding a
CC protein comprising: (i) a base sequence in which 1-20 bases are deleted,
CC replaced or added in AAH21757; or (ii) at least one base is deleted,
CC or replaced or added in a fully defined 519 base sequence (AAH21768), and
CC having molecular chaperone activity in (i). Also described is a method
CC for the preparation of L-glutamic acid by fermentation in which the
CC transformed (I) is used and cultured at a high temperature limiting the
CC production of L-glutamic acid with the untransformed (I). The microbe can
CC be used for the preparation of L-glutamic acid. The present sequence
CC represents a PCR primer used in the preparation of *Corynebacterium*
CC glutamicum chaperone CpkB, which is used in an example from the present
CC invention
XX
SQ Sequence 27 BP; 4 A; 9 C; 8 G; 6 T; 0 U; 0 Other;

Query Match 66.0%; Score 13.2; DB 4; Length 27;
Best Local Similarity 83.3%; Pred. No. 1.6e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 GACGCGCGCTCGTTCAT 20
Db 9 GACGCGCGCAACGCCAT 26

RESULT 11
AAV51704/c
ID AAV51704 standard; DNA; 21 BP.
XX
AC AAV51704;
XX
DT 02-FEB-1999 (first entry)
XX
DE Zea mays genome forward PCR primer #304.
XX
KW Polymorphic marker; allele-specific; probe; amplification; PCR primer;
KW hybridisation; plant; hybrid certification; genetic contribution;
KW progeny; back-cross; hybrid; ancestry; corn; ss.
XX
OS Synthetic.
OS Zea mays.
XX
FN WO9824796-A1.
XX
PD 11-JUN-1998.
XX
PF 01-DEC-1997; 97WO-US021782.
XX
PR 02-DEC-1996; 96US-0032069P.
PR 07-MAR-1997; 97US-00813507.
XX
PA (AFFY-) AFFYMETRIX INC.
XX
PI Lenieux B, Landry BS, Sapolsky RJ, Murigneux A;
XX
DR WPI; 1998-333252/29.
XX
FT Brassica species allele-specific oligonucleotide probes and primers -
FT useful for plant breeding.
XX
PS Example 1; Page 55; 65pp; English.
XX
CC AAV51401-V51704 are forward PCR primers used to amplify fragments of the
CC Zea mays genome in order to detect polymorphic markers. Such markers can
CC be used in the construction of allele-specific primers and probes for
CC amplification or hybridisation, e.g. to determine common or disparate
CC ancestry between 2 or more plants, to monitor the genetic contribution of
CC an ancestral plant, to trace the progeny of proprietary plants, in
CC certification of a hybrid plant or to identify the progeny of a back-
CC crossed plant with an ancestral plant
XX
SQ Sequence 21 BP; 3 A; 11 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 64.0%; Score 12.8; DB 2; Length 21;
Best Local Similarity 87.5%; Pred. No. 2.4e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGGACGCGCGCTCGG 16
Db 16 GGGACGCGCGCTCGG 1

RESULT 12
AAA75395/c
ID AAA75395 standard; DNA; 23 BP.
XX
AC AAA75395;
XX
DT 15-JAN-2001 (first entry)
XX
DE Fragment derived from the origin of replication of pBR322.
XX
KW pBR322 plasmid; probe; primer; origin of replication;
KW gene therapy vector; ss.
XX
OS Synthetic.
XX
PN WO200053803-A1.
XX
PD 14-SEP-2000.
XX
PF 03-MAR-2000; 2000WO-FR000543.
XX
PR 05-MAR-1999; 99FR-00002968.
XX
PA (TRGE) TRANSGENE.
XX
PI Lamy D;
XX
DR WPI; 2000-587445/55.
XX
PT Nucleic acid sequences that hybridize to the pBR322 origin of
PT replication, useful for monitoring gene therapy vectors, and as probes or
PT primers.
XX
PS Claim 3; Page 26; 36pp; French.
XX
CC AAA75311-41 and AAA75393-A75402 are derived from the origin of
CC replication of the pBR322 plasmid. The nucleic acid fragments are useful
CC as probes and primers for detecting sequences derived from the origin of
CC replication of pBR322 or vectors (or their fragments) that contain such
CC sequences. They are particularly used to monitor the presence of gene
CC therapy vectors (used to deliver therapeutic genes or proteins, antisense
CC sequences or ribozymes), e.g. for determining disappearance of the
CC vector, for adjustment of treatment, or for timing of new treatments.
CC They can also be used to screen foods and cosmetics for the presence of
CC derived materials from genetically modified organisms
XX
SQ Sequence 23 BP; 6 A; 7 C; 8 G; 2 T; 0 U; 0 Other;

Query Match 64.0%; Score 12.8; DB 3; Length 23;
Best Local Similarity 87.5%; Pred. No. 2.4e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 CGCGCGCGCTCGTTCAT 20
Db 16 CGCTGCGCTCGGTGCT 1

RESULT 13
ABZ58873
ID ABZ58873 standard; DNA; 24 BP.
XX
AC ABZ58873;
XX

PF 14-NOV-2003; 2003MO-US036611.
XX
PR 14-NOV-2002; 2002US-0426144P.
PR 21-FEB-2003; 2003US-00371913.
PR 28-JUN-2003; 2003US-00608577.
PR 21-JUL-2003; 2003US-0489095P.
PR 25-AUG-2003; 2003US-0497644P.
PR 28-OCT-2003; 2003US-0515175P.
PR 14-NOV-2003; 2003US-00713653.
XX
PA (THIR-) THIRD WAVE TECHNOLOGIES INC.
XX
PI Accola M, Wigdal SS, Mast AL, Bartholomay CT, Kwiatkowski RW;
PI Tevere V, Ip HS, Carroll K, Peterson P, Agarwal P, Jarvis N;
PI Hall JG, Heisler L;
XX
DR WPI; 2004-420702/39.
XX
PT Detecting Cystic Fibrosis Transmembrane Conductance Regulator (CFTR)
PT alleles, useful for screening mutations associated with cystic fibrosis,
PT comprises exposing amplified CFTR target nucleic acid to detection
PT assays.
XX
XX Example 7; SEQ ID NO 169; 147pp; English.
XX
CC The invention relates to detecting Cystic Fibrosis Transmembrane
CC Conductance Regulator (CFTR) alleles comprising providing a sample
CC comprising a CFTR target nucleic acid, amplifying the CFTR target nucleic
CC acid with 25 cycles or fewer of a PCR to generate amplified target
CC nucleic acid, and exposing the amplified target nucleic acid to detection
CC assays configured to detect CFTR alleles under conditions such that the
CC presence or absence of the CFTR alleles is detected, using an invasive
CC cleavage structure assay (designated INVADER), employing FRET probes
CC (fluorescent resonance energy transfer). Also included is a kit
CC comprising a non-amplified oligonucleotide detection assay configured for
CC detecting at least one CFTR allele or oligonucleotide detection assays
CC configured for detecting a set of CFTR alleles where the set is a first
CC set comprising 2789+5G to A, R1162X, R560T, 1898+1 G to A, del1507,
CC 1148T, and A455E, a second set comprising 3120+1G to A, 3659delC, G551D,
CC N1303K, 1078delT, R334W, 711+1G to T, and 3849+10kb, a third set
CC comprising 621+1G to T, W1282X, 1717-1G to A, and R117H, or a fourth set
CC comprising R347P, G85E, G542X and R553X, or a fifth set comprising
CC 2184delA. The non-amplified oligonucleotide detection assay or the
CC oligonucleotide detection assays comprises first and second
CC oligonucleotides configured to form an invasive cleavage structure in
CC combination with a target sequence comprising the CFTR allele. The first
CC oligonucleotide comprises a 5' portion and a 3' portion, where the 3'
CC portion is configured to hybridise to the target sequence and the 5'
CC oligonucleotide comprises a 5' portion and a 3' portion, where the 5'
CC portion is configured to hybridise to the target sequence and the 3'
CC portion is configured to not hybridise to the target sequence. The method
CC and kit are useful for detecting CFTR alleles, more particularly for
CC screening nucleic acid samples e.g. from patients, for the presence of
CC any one of a collection of mutations in the CFTR gene associated with
CC cystic fibrosis. The method and compositions are useful for generating
CC and analysing limited cycle, multiplexed amplification of a large
CC collection of CFTR loci. The present sequence comprises a probe for the
CC method of the invention detecting the wild-type CFTR allele.
XX
SQ Sequence 29 BP; 6 A; 9 C; 9 G; 5 T; 0 U; 0 Other;

Query Match 64.0%; Score 12.8; DB 12; Length 29;
Best Local Similarity 87.5%; Pred. No. 2.4e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GGACGGCGGCTCGGT 17
| | | | | | | | | |
Db 3 GGACGGCGGCTCAGT 18

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OM nucleic - nucleic search, using sw model

Run on: November 27, 2005, 04:44:55 ; Search time 3610 Seconds
(without alignments)
259.208 Million cell updates/sec

Title: US-10-605-498-82

Perfect score: 20

Sequence: 1 gggacgcgcgtcgatc 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 76294

Minimum DB seq length: 12

Maximum DB seq length: 35

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: gb_est1:*

2: gb_est2:*

3: gb_est3:*

4: gb_hic:*

5: gb_est4:*

6: gb_est5:*

7: gb_est6:*

8: gb_est7:*

9: gb_gss1:*

10: gb_gss2:*

11: gb_gss3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	12.8	64.0	32	2	BF131807 601820724
C 2	12.4	62.0	26	10	AG203073 Pan trogl
C 3	12.2	61.0	28	1	AI287864 qv07d12.x
C 4	12	60.0	31	1	AA867755 vx16b08.r
C 5	11.4	60.0	31	10	CZ169504 G050C04 G
C 6	11.4	57.0	31	9	AZ826864 2M0102H20
C 7	11.2	56.0	23	10	AJ587908 Arabidops
C 8	11.2	56.0	31	6	CD028820 mgmy006xa
C 9	11	55.0	21	9	AZ420773 1M0198E18
C 10	11	55.0	33	10	AJ599957 Arabidops
C 11	11	55.0	34	1	AA259780 va87b10.r
C 12	10.6	53.0	25	1	AI758887 ty94c11.x
C 13	10.6	53.0	25	6	CF643223 D61 D08 F
C 14	10.6	53.0	29	6	CF643257 D62-B05 F
C 15	10.6	53.0	33	10	AG216212 drosophil
C 16	10.6	53.0	35	6	CF298077 7LEAF--01
C 17	10.6	53.0	35	6	CF642505 D52 E05 F
C 18	10.6	53.0	35	3	DR108402 JHU163B05
C 19	10.4	52.0	22	8	BM398778 5009-0-5-
C 20	10.4	52.0	26	10	CG731752 1119143B1
C 21	10.4	52.0	27	11	TA103C01P
C 22	10.4	52.0	28	1	AI256473 ui86g06.x

23	10.4	52.0	29	9	CC456807	CC456807 SALK_1007
C 24	10.4	52.0	31	10	CG724391	CG724391 1119081A0
25	10.4	52.0	34	8	N55046	N55046 yz20g11.r1
26	10.4	52.0	34	9	AZ346691	AZ346691 1M0082103
C 27	10.2	51.0	25	1	AI002379	AI002379 qcr87f02.8
C 28	10.2	51.0	27	6	CF277108	CF277108 14ETL--02
C 29	10.2	51.0	28	1	AB080287	AB080287 AB080287
C 30	10.2	51.0	28	1	AI358659	AI358659 qx60807.x
C 31	10.2	51.0	29	1	AW246529	AW246529 2821891.3
C 32	10.2	51.0	30	1	AJ746806	AJ746806 AJ746806
C 33	10.2	51.0	30	10	CZ472135	CZ472135 d01278-5p
34	10.2	51.0	31	1	AA912813	AA912813 o143b02.8
35	10.2	51.0	31	3	BI915569	BI915569 603176924
C 36	10.2	51.0	33	10	AJ600534	AJ600534 Arabidops
C 37	10.2	51.0	33	11	DME545177	AJ545177 Drosophil
38	10.2	51.0	34	1	AA737625	AJ737625 oa52c01.8
39	10.2	51.0	34	10	CG712020	CG712020 1119023G0
40	10	50.0	21	9	AZ513847	AZ513847 1M0360D08
41	10	50.0	22	8	DR103042	DR103042 JHU009E01
42	10	50.0	27	9	AZ769255	AZ769255 1M0569B17
43	10	50.0	30	1	AJ746842	AJ746842 AJ746842
C 44	10	50.0	30	10	CZ472687	CZ472687 d02227-3p
C 45	10	50.0	30	10	CZ488898	CZ488898 f06234-5p

ALIGNMENTS

RESULT 1	BF131807/c	BF131807	32 bp	mRNA	linear	EST 24-OCT-2000
LOCUS	601820724F1	NIH_MGC_58	Homo sapiens	cDNA	clone	IMAGE:4052596 5',
DEFINITION	mRNA sequence.					
ACCESSION	BF131807.1	GI:10970847				
VERSION	BF131807					
KEYWORDS	EST.					
SOURCE	Homo sapiens (human)					
ORGANISM	Homo sapiens					
REFERENCE	1 (bases 1 to 32)					
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/ .					
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)					
JOURNAL	Unpublished (1999)					
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cga@bbs-r@mail.nih.gov Tissue Procurement: ATCC					

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.llnl.gov>
Plate: L1CM889 row: p column: 05
High quality sequence start: 8
High quality sequence stop: 30.
Location/Qualifiers
1..32
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4052596"
/tissue_type="hypernephroma"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH_MGC_58"
/note="Organ: Kidney; Vector: pNR-LIB (Clontech); Site_1: Sfil (ggcgctcgcc); Site_2: Sfil (ggcgctcgcc); Double-stranded cDNA was prepared from cell line RNA. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CAGGCCATTATGCG-3' and 3' adaptor sequence: 5'-ATTCTAGAGCGGCGCCGACATG-dT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average

FEATURES
source

insert size 1.35 kb (range 0.9-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA)."

ORIGIN

Query Match 64.0%; Score 12.8; DB 2; Length 32;
Best Local Similarity 87.5%; Pred. No. 2.5e+05;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 CGGCGCGCTCGGTCAT 20
|||||
Db 27 CGCTGCGCTCGGTCGT 12

RESULT 2
AG203073
LOCUS
DEFINITION Pan troglodytes DNA, clone: RP43-087B01.T7, genomic survey
AG203073 26 bp DNA linear GSS 06-MAR-2004
sequence.

ACCESSION
VERSION AG203073.1 GI:45235248
KEYWORDS GSS.

SOURCE Pan troglodytes (chimpanzee)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Pan.

REFERENCE
AUTHORS Park,H., Kim,Y., Kim,S., Han,Y., Woo,T., Park,K., Eun,C.J.,
Hoon,S.T., Chu,M., Kim,H., Joo,S., Kim,C., Song,W. and Yoo,H.
BAC end sequences of Library RP-43

JOURNAL Unpublished
AUTHORS
TITLE 2 (bases 1 to 26)
JOURNAL

REFERENCE
AUTHORS Park,H., Kim,Y., Kim,S., Han,Y., Woo,T., Park,K., Eun,C.J.,
Hoon,S.T., Chu,M., Kim,H., Joo,S., Kim,C., Song,W. and Yoo,H.
Direct Submission
Submitted (07-JAN-2002) Hong-Seog Park, Korea Research Institute of
Bioscience and Biotechnology (KRIIB), Genome Research Center (GRC);
52, Oun-dong, Yusong-gu, Daejeon 305-333, Korea
(E-mail:redstone@mail.kribb.re.kr, URL:http://phs.grc.kribb.re.kr/,
Tel:82-42-866-7181, Fax:82-42-860-4409)

COMMENT Clones are derived from the chimpanzee BAC library RP-43 This BAC
end was generated during the R&D process and may have higher chance
of clone tracking errors.

PRIMERS

Sequencing: T7

LIBRARY
Vector : pBACe3.6
R.Site 1 : EcoRI
R.Site 2 : EcoRI.

FEATURES
source
1..26
Location/Qualifiers
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
/clones="RP43-087B01.T7"
/sex="male"
/cell_type="lymphocytes"
/clone_lib="RP-43 Chimpanzee Male BAC Library"

Query Match 62.0%; Score 12.4; DB 10; Length 26;
Best Local Similarity 92.9%; Pred. No. 3.9e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGGACGGCGGCTC 14
|||||
Db 1 GGGACTGGCGCTC 14

RESULT 3
AI287864/c

LOCUS
DEFINITION AI287864 28 bp mRNA linear EST 24-NOV-1998
QV07d12.x1 NCI CGAP Kid8 Homo sapiens cDNA clone IMAGE:1980887 3'
similar to SW-CA44 HUMAN P53420 COLLAGEN ALPHA 4(IV) CHAIN
PRECURSOR. ; contains MER22.B3 TAR1 repetitive element ;, mRNA
sequence.

ACCESSION
VERSION AI287864.1 GI:3927617
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.

REFERENCE 1 (bases 1 to 28)

AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

JOURNAL Unpublished (1997)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality

Seq primer: -40UP from Gibco

High quality sequence stop: 1.

FEATURES
source

1..28
Location/Qualifiers

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:1980887"

/issue_type="renal cell tumor"

/lab_host="DH10B"

/clone_lib="NCI-CGAP Kid8"

/notes="Organ: Kidney; Vector: pCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.

Average insert size 1.2 kb. Life Technologies catalog #:

11524-014"

ORIGIN

Query Match 61.0%; Score 12.2; DB 1; Length 28;
Best Local Similarity 82.4%; Pred. No. 4.7e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GGGACGGCGGCTCGGT 17
|||||
Db 21 GGGCGGGCGGCGCGGT 5

RESULT 4

AA867755/c

LOCUS

DEFINITION AA867755 31 bp mRNA linear EST 16-MAR-1998
vx16b08.r1 Soares_thymus_2NDMT Mus musculus cDNA clone
IMAGE:1264599 5', similar to TR:O35394 O35394 PRENYLATED RAB
ACCEPTOR 1. ;, mRNA sequence.

ACCESSION
VERSION AA867755.1 GI:2963200
KEYWORDS EST.
SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 31)

AUTHORS Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisels,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,

Contact: GGTC
German Genetrapp Consortium (GGTC)
Email: info@genetrapp.de
U3CEO gene trap. Sequence tag generated by 5'RACE. Additional
sequence information can be found at:
'http://genetrapp.gsf.de/project/web_new/database/result_clone.html?
clone_id=G050C04'. ES cell line harboring insertion mutation of
target gene is available at:
'http://genetrapp.gsf.de/project/web_new/order_clones/howtoorder.htm#
1'. Inhouse Sequence Identifier: 16629
Class: Gene Trap.

FEATURES
source Location/Qualifiers
1..31
/organism="Mus musculus"
/mol_type="mRNA"
/strain="129 Sv"
/db_xref="taxon:10090"
/clone="G050C04"
/sex="Male"
/cell_type="Embryonic stem cell"
/cell_line="ES cells (C57BL/6J x 129Sv/SvEVtac) F1"
/clone_lib="GGTC Gene Trap Library GV07C05"
/note="Vector: U3CEO"

ORIGIN
Query Match 60.0%; Score 12; DB 10; Length 31;
Best Local Similarity 75.0%; Pred. No. 5.7e+05;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GGGACGGGGCGTCTGGTCAT 20
||||| ||||| |||||
Db 29 GGGACGGGGCGGTGCACAT 10
||||| ||||| |||||

RESULT 6
AZ826864
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

REFERENCE
AUTHORS

TITLE

JOURNAL
COMMENT

AZ826864
2M0102H20R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0102H20 R, genomic survey sequence.
AZ826864
AZ826864.1 GI:12996772
GSS.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Muridae; Murinae; Mus.
1 (bases 1 to 31)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0102 row: H column: 20
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 31.
Location/Qualifiers
1..31
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"

```

/db_xref="taxon:10090"
/clone="UUGC2M0102H20"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 [gi14732114|gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN
Query Match 57.0%; Score 11.4; DB 9; Length 31;
Best Local Similarity 92.3%; Pred. No. 1.1e+06;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGGACGGCGGCT 13
|||||
Db 19 GGGACGGCGGCT 31

RESULT 7
AJ587908/c
LOCUS
DEFINITION
Arabidopsis thaliana T-DNA flanking sequence, left border, clone 339B10, genomic survey sequence.
AJ587908
VERSION
AJ587908.1 GI:37937532
KEYWORDS
GSS; left border; T-DNA flanking sequence.
SOURCE
Arabidopsis thaliana (thale cress)
ORGANISM
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.

REFERENCE
1
AUTHORS
Brunaud, V., Balzerque, S., Dubreucq, B., Aubourg, S., Samson, F., Chauvin, S., Bechtold, N., Cruaud, C., Derose, R., Pelletier, G., Lepiniec, L., Caboche, M., and Leclercq, A.
TITLE
T-DNA integration into the Arabidopsis genome depends on sequences of pre-insertion sites
JOURNAL
EMBO Rep. 3 (12), 1152-1157 (2002)
PUBMED
12446565
REFERENCE
2 (bases 1 to 23)
AUTHORS
Balzerque, S.
TITLE
Direct Submission
JOURNAL
Submitted (23-OCT-2003) Balzerque S., UMRGV, INRA/CNRS, 2 rue Gaston Cremieux, 91057 Evry cedex, FRANCE
COMMENT
PCR was performed on DNA from transformants of Arabidopsis thaliana plants from INRA (Versailles). The DNA fragment (e) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at http://dbgap.versailles.inra.fr/publiclines/. This sequence has been generated in the framework of the French plant genomics program 'genoplante' (http://www.genoplante.com and http://genoplante-info.inbio.gen.fr).
FEATURES
Location/Qualifiers

source
1..23
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/db_xref="taxon:3702"
/clone="339B10"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
/ecotype="Wassilewskija"
misc_feature
1..23
/notes="T-DNA flanking sequence
left border"

ORIGIN
Query Match 56.0%; Score 11.2; DB 10; Length 23;
Best Local Similarity 81.2%; Pred. No. 1.4e+06;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GGGACGGCGGCTCGG 16
|||||
Db 21 GGGACGCGCGCATGG 6

RESULT 8
CD028820
LOCUS
DEFINITION
grisea cDNA clone mgmy006xA17 5', mRNA sequence.
CD028820
VERSION
CD028820.1 GI:30410276
KEYWORDS
EST.
SOURCE
Magnetoporthes grisea (anamorph: Pyricularia grisea)
ORGANISM
Magnetoporthes grisea
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariomycetes incertae sedis; Magnetoporthaceae; Magnetoporthes.

REFERENCE
1 (bases 1 to 31)
AUTHORS
Ebbole, D.J., Yuan, J., Thomas, T.L., Bobrowicz, P., Lu, G., Shatterai, K., and Dean, R.A.
TITLE
Expressed sequence tags from the rice blast fungus, Magnetoporthes grisea
JOURNAL
Unpublished (2002)
COMMENT
Contact: Ebbale DJ
Department of Plant Pathology & Microbiology
Texas A&M University
Peterson Bldg, MS2132, College Station, TX 77843-2132, USA
Tel: 979 845 4831
Fax: 979 845 6483
Email: d-ebbale@tamu.edu
Chromatogram file of this sequence is available, see contact person;
PCR Primers
FORWARD: T3 primer
BACKWARD: T7 primer
Plate: mgmy006 row: A column: 17
Seq primer: T3.
FEATURES
Location/Qualifiers

source
1..31
/organism="Magnetoporthes grisea"
/mol_type="mRNA"
/strain="70-15"
/db_xref="taxon:148305"
/clone="mgmy006xA17"
/sex="Mat1-2 hermaphrodite"
/cell_type="mycelium"
/clone_lib="Magnetoporthes grisea MY Uni-Zap XR Library"
/notes="Vector: pBluescriptSK+; Site 1: EcoRI; Site 2: XhoI; Unidirectional cloning. EcoRI site has T3 primer and predominantly 5' reads. T7 primer on XhoI side of insert. Minimal medium mycelium library. Sequences were processed by one of two methods. Where a full-length alignment to the M. grisea genome sequence was available, the EST sequence was trimmed according to the alignment, otherwise sequence quality was assessed using phredPhrap version 991019 and trimmed according to phd files (0.05) and for vector seqs."

```

ORIGIN

Query Match 56.0%; Score 11.2; DB 6; Length 31;
 Best Local Similarity 81.2%; Pred. No. 1.3e+06;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 CGCGGCGCTCGGTCAAT 20
 | | | | | | | | | |
 Db 6 CTCGGCGTTTGGTCAAT 21

RESULT 9

AZ420773/c

LOCUS AZ420773 21 bp DNA linear GSS 03-OCT-2000
 DEFINITION IM0198E18R Mouse 10kb plasmid UGCG1M library Mus musculus genomic
 clone UGCG1M0198E18 R, genomic survey sequence.

ACCESSION AZ420773

VERSION AZ420773.1 GI:10544786

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 21)
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
 Niederhausern,A. and Wright,D. Weiss,R.

TITLE

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

COMMENT Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0198 row: E column: 18

Seq primer: CACACGGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 21.

Location/Qualifiers

1..21

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UGCG1M0198E18"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, P-"

/clone_lib="Mouse 10kb plasmid UGCG1M library"

/notes="vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of pWB42 (gi|4732114|gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and

purified. The sheared, adapted mouse DNA was annealed to

adapted vector DNA, and transformed into

chemically-competent E. coli XL10-Gold (Stratagene) cells

ORIGIN

Query Match 55.0%; Score 11; DB 9; Length 21;
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGACGCGCGC 11
 | | | | | | | | | |
 Db 16 GGGACGCGCGC 6

RESULT 10

AJ599957

LOCUS AJ599957

DEFINITION Arabidopsis thaliana T-DNA flanking sequence, left border, clone
 497C08, genomic survey sequence.

ACCESSION AJ599957.1 GI:37949585

VERSION GSS; left border; T-DNA flanking sequence.

KEYWORDS Arabidopsis thaliana (thale cress)

SOURCE Arabidopsis thaliana

ORGANISM Arabidopsis thaliana

REFERENCE 1
 AUTHORS Brunaud,V., Balzerque,S., Dubreucq,B., Aubourg,S., Samson,F.,
 Chauvin,S., Bechtold,N., Cruaud,C., DeRose,R., Pelletier,G.,
 Lepiniec,L., Caboche,M. and Lecharny,A.

TITLE

T-DNA integration into the Arabidopsis genome depends on sequences

of pre-insertion sites

EMBO Rep. 3 (12), 1152-1157 (2002)

REFERENCE 2 (bases 1 to 33)

AUTHORS Balzerque,S.

JOURNAL Direct Submission

COMMENT Submitted (23-OCT-2003) Balzerque S., UMRGV, INRA/CNRS, 2 rue

Gaston Cremieux, 91057 Evry cedex, FRANCE

PCR was performed on DNA from transformants of Arabidopsis thaliana

plants from INRA (Versailles). The DNA fragment(s) resulting from

the PCR were directly sequenced from the left or the right border

to determine the genomic sequence flanking the insertion. T-DNA

derived sequences were removed. Information to order the

corresponding mutant line and a link to a database providing a

graphical display of the insertion site are available at

http://dbgap.versailles.inra.fr/publiclines/. This sequence has

been generated in the framework of the French plant genomics

program 'Genoplante' (http://www.genoplante.com and

http://genoplante-info.infobiogen.fr).

Location/Qualifiers

1..33

/organism="Arabidopsis thaliana"

/mol_type="genomic DNA"

/db_xref="taxon:3702"

/clone="497C08"

/clone_lib="Arabidopsis thaliana T-DNA insertion lines"

/ecotype="Wassilewskija"

misc_feature 1..33

/note="T-DNA flanking sequence

left border"

ORIGIN

Query Match 55.0%; Score 11; DB 10; Length 33;

Best Local Similarity 100.0%; Pred. No. 1.6e+06;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGACGCGCGC 11

| | | | | | | | | |

Db 23 GGGACGCGCGC 33

| | | | | | | | | |

RESULT 11

AJ599957/c

and selected for ampicillin resistance."

LOCUS AA259780 34 bp mRNA linear EST 18-MAR-1997
 DEFINITION vab7b10.r1 Soares mouse 3NWE12.5 Mus musculus cDNA clone
 IMAGE:746395.5' similar to TR:G971986 G971986 NADH DEHYDROGENASE ;,
 mRNA sequence.

ACCESSION AA259780
 VERSION AA259780.1 GI:1896266
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 34)
 AUTHORS Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Stepien,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.

TITLE The WashU-HHMI Mouse EST Project
 JOURNAL Unpublished (1996)
 COMMENT Contact: Marra M/Mouse EST Project
 WashU-HHMI Mouse EST Project
 Washington University School of MedicineP
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@wustl.edu
 This clone is available royalty-free through LLNL ; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 MGI:455379

Trace considered overall poor quality
 Possible reversed clone: similarity on wrong strand
 Seq primer: -28ml3 rev2 ET from Amersham
 High quality sequence stop: 1.
 Location/Qualifiers
 1..34
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="IMAGE:746395"
 /sex="unknown"
 /tissue_type="fetus"
 /dev_stage="12.5dpc total fetus"
 /lab_host="DH10B"
 /clone_lib="Soares mouse 3NWE12.5"
 /notes="Organ: whole fetus; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site.1: Not I; Site.2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5', TGTTACCAATCTGAAGTGGAGCGCGCTTATTTTTTTTTTTTTTTT 3'], on total mouse RNA [provided by Minoru Ko, Wayne State Univ.]; double-stranded cDNA was ligated to Eco RI adaptors [Pharmacia], digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Patima Bonaldo. "

Query Match 55.0%; Score 11; DB 1; Length 34;
 Best Local Similarity 73.7%; Pred. No. 1.6e+06;
 Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GGGACGGCGCTCGGTCA 19
 ||||| ||||| ||||| |||||
 Db 34 GGGACTAGCTCATGGTCA 16

RESULT 12
 LOCUS AA1758887 25 bp mRNA linear EST 23-JUN-1999
 DEFINITION ty94c11.x1 NCI CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2286740 3', similar to TR:Q64371 Q64371 PR-VBETA1. ;contains element TAR1 repetitive element ;, mRNA sequence.

ACCESSION AI758887
 VERSION AI758887.1 GI:5152612
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 25)
 AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgaps-r@mail.nih.gov
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
 CDNA Library Preparation: Life Technologies, Inc.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
 www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
 Seq primer: -40UP from Gibco
 High quality sequence stop: 1.
 Location/Qualifiers
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 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:2286740"
 /tissue_type="well-differentiated endometrial adenocarcinoma, 7 pooled tumors"
 /lab_host="DH10B"
 /clone_lib="NCI CGAP_Ut1"
 /notes="Organ: uterus; Vector: pCMV-SPORT6; Site.1: SalI; Site.2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.75 kb. Life Technologies catalog #: 11538-014"

Query Match 53.0%; Score 10.6; DB 1; Length 25;
 Best Local Similarity 76.5%; Pred. No. 2.5e+06;
 Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GGGACGGCGCTCGGT 17
 ||||| ||||| ||||| |||||
 Db 5 GGGGGGGCGCGCCCGGT 21

RESULT 13
 LOCUS CF643223/c 25 bp mRNA linear EST 02-OCT-2003
 DEFINITION D61.D08 Filamentous Forced Diploid Ustilago maydis cDNA 3', mRNA sequence.

ACCESSION CF643223
 VERSION CF643223.1 GI:37411328
 KEYWORDS EST.
 SOURCE Ustilago maydis
 ORGANISM Ustilago maydis

REFERENCE 1 (bases 1 to 25)
 AUTHORS Nugent,K.G., Choffe,K. and Saville,B.J.
 TITLE Gene expression during Ustilago maydis diploid filamentous growth: EST library creation and analyses
 JOURNAL Fungal Genet. Biol. 41 (3), 349-360 (2004)
 PUBMED 14761795
 COMMENT Contact: Barry J. Saville
 Saville Lab
 University of Toronto

3359 Mississauga Road North, Mississauga, ON, L5L 1C6, Canada
Tel: 905 569 4702
Fax: 905 828 3792
Email: bsaville@utm.utoronto.ca
Plate: UTM-UM-D126/7-061-UTM row: 08 column: D
Seq primer: T7 Reverse (5' GAGTAATACGACTACTATAGG 3')
High quality sequence stop: 25.
Location/Qualifiers

FEATURES
source

1. .25
/organism="Ustilago maydis"
/mol_type="mRNA"
/strain="PBD12"
/db_xref="taxon:5270"
/cell_type="Mycelia"
/dev_stage="Filamentous diploid"
/clone_lib="Filamentous Forced Diploid"
/notes="Vector: pSport; mRNA was extracted from diploid mycelia. A cDNA library was constructed and unidirectionally cloned into pSPORT plasmid, with the use of the Superscript II cDNA Library Construction Kit."

ORIGIN

Query Match 53.0%; Score 10.6; DB 6; Length 25;
Best Local Similarity 76.5%; Pred. No. 2.5e+06;
Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 GGACGGCGCTCGGTC 18
||||| | ||| ||
Db 24 GGACGGTGGTGCATC 8

RESULT 14

CF643257/c
LOCUS
DEFINITION
Dc2_B05 Filamentous Forced Diploid Ustilago maydis cDNA 3', mRNA
sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

CF643257 1 GI:37411392
Ustilago maydis
Ustilago maydis
Eukaryota; Fungi; Basidiomycota; Ustilaginomycetes;
Ustilaginomycetidae; Ustilaginales; Ustilaginaceae; Ustilago.
1 (bases 1 to 29)
Nugent, K.G., Choffe, K. and Saville, B.J.
Gene expression during Ustilago maydis diploid filamentous growth:
EST library creation and analyses
Fungal Genet. Biol. 41 (3), 349-360 (2004)
14761795

Contact: Barry J. Saville
Saville Lab

University of Toronto
3359 Mississauga Road North, Mississauga, ON, L5L 1C6, Canada
Tel: 905 569 4702

Fax: 905 828 3792
Email: bsaville@utm.utoronto.ca
Plate: UTM-UM-D126/7-062-UTM row: 05 column: B
Seq primer: T7 Reverse (5' GAGTAATACGACTACTATAGG 3')
High quality sequence stop: 29.
Location/Qualifiers

FEATURES
source

1. .29
/organism="Ustilago maydis"
/mol_type="mRNA"
/strain="PBD12"
/db_xref="taxon:5270"
/cell_type="Mycelia"
/dev_stage="Filamentous diploid"
/clone_lib="Filamentous Forced Diploid"
/notes="Vector: pSport; mRNA was extracted from diploid mycelia. A cDNA library was constructed and unidirectionally cloned into pSPORT plasmid, with the use of the Superscript II cDNA Library Construction Kit."

ORIGIN

Query Match 53.0%; Score 10.6; DB 6; Length 29;
Best Local Similarity 76.5%; Pred. No. 2.5e+06;
Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 GGACGGCGCTCGGTC 18
||||| | ||| ||
Db 28 GGACGGTGGTGCATC 12

RESULT 15

AG216212/c
LOCUS
DEFINITION
Drosophila melanogaster DNA, clone:NP1197-5-1, flanking P[GawB]
transposon insertion, genomic survey sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

AG216212 1 GI:22763212
GSS.
Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.

REFERENCE

AUTHORS
Hayashi, S., Ito, K., Sado, Y., Taniguchi, M., Akimoto, A., Takeuchi, H.,
Aigaki, T., Matsuzaki, F., Nakagoshi, H., Tanimura, T., Ueda, R.,
Uemura, T., Yoshihara, M. and Goto, S.

GETDB, a database compiling expression patterns and molecular
locations of a collection of Gal4 enhancer traps
Genesis (2002) in press
2 (bases 1 to 33)

JOURNAL

REFERENCE

AUTHORS

TITLE

Submitted (27-AUG-2002) Shigeo Hayashi, RIKEN Center for
Developmental Biology, Laboratory for Morphogenetic Signaling;
Chuo-ku, Minatojima-minamimachi 2-2-3, Kobe, Hyogo 650-0047, Japan
(E-mail: shayashi@cdb.riken.go.jp, Tel: 81-78-301-3184,
Fax: 81-78-301-3183)

COMMENT
This clone was isolated from genomic DNA flanking an insertion of
the P element vector P[GawB] of a Drosophila strain.

FEATURES
source

1. .33
Location/Qualifiers
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/strain="NP1197"
/db_xref="taxon:7227"
/chromosome="2"
/map="54C6"
/clone="NP1197-5-1"
/note="flanking P[GawB] transposon insertion"

ORIGIN

Query Match 53.0%; Score 10.6; DB 10; Length 33;
Best Local Similarity 76.5%; Pred. No. 2.4e+06;
Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 GGACGGCGCTCGGTC 18
||||| | ||| ||
Db 22 GCACGCTGCACGGTC 6

Search completed: November 27, 2005, 06:30:03
Job time : 3611 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 27, 2005, 04:52:55 ; Search time 135 Seconds
(without alignments)
263.342 Million cell updates/sec

Title: US-10-605-498-82

Perfect score: 20

Sequence: 1 gggacgcgctcgatc 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 1065270

Minimum DB seq length: 12

Maximum DB seq length: 35

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA.*

- 1: /cgn2_6/ptodata/1/ina/1 COMB.seq.*
- 2: /cgn2_6/ptodata/1/ina/5 COMB.seq.*
- 3: /cgn2_6/ptodata/1/ina/6A COMB.seq.*
- 4: /cgn2_6/ptodata/1/ina/6B COMB.seq.*
- 5: /cgn2_6/ptodata/1/ina/H COMB.seq.*
- 6: /cgn2_6/ptodata/1/ina/PCTUS COMB.seq.*
- 7: /cgn2_6/ptodata/1/ina/PP COMB.seq.*
- 8: /cgn2_6/ptodata/1/ina/RE COMB.seq.*
- 9: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
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C 3	13.8	69.0	25	3	US-09-396-196G-46323
C 4	13.8	69.0	25	3	US-09-396-196G-46324
C 5	13.8	69.0	25	3	US-09-396-196G-46335
C 6	13.2	66.0	25	3	US-09-396-196G-53301
7	13	65.0	20	3	US-09-466-858A-19
8	13	65.0	20	3	US-09-450-515-19
9	13	65.0	20	3	US-10-206-654-19
10	12.6	63.0	20	3	US-10-131-827-8773
C 11	12.6	63.0	24	3	US-09-540-014-35
C 12	12.6	63.0	24	3	US-09-164-210-12
C 13	12.6	63.0	24	3	US-09-538-864-14
C 14	12.6	63.0	24	3	US-10-091-841A-35
C 15	12.6	63.0	25	3	US-09-396-196G-40648
C 16	12.6	63.0	30	3	US-09-319-648-52
17	12.6	63.0	30	9	5240848-8
18	12.4	62.0	20	2	US-08-182-175A-9
19	12.4	62.0	20	2	US-08-474-633A-16
20	12.4	62.0	20	3	US-08-823-771-16
21	12.4	62.0	20	6	PCT-US92-06412-9
C 22	12.4	62.0	25	3	US-09-396-196G-41065
C 23	12.4	62.0	25	3	US-09-396-196G-46162
C 24	12.4	62.0	25	3	US-09-396-196G-46163

25	12.2	61.0	21	3	US-09-158-863C-38	Sequence 38, Appl
C 26	12.2	61.0	22	3	US-09-589-560B-58	Sequence 58, Appl
C 27	12.2	61.0	22	3	US-09-589-560B-62	Sequence 62, Appl
C 28	12.2	61.0	25	3	US-09-396-196G-25195	Sequence 25195, A
C 29	12.2	61.0	25	3	US-09-396-196G-49392	Sequence 49392, A
C 30	12.2	61.0	34	3	US-09-487-558B-3	Sequence 3, Appli
C 31	12	60.0	23	3	US-09-462-671-1	Sequence 1, Appli
C 32	12	60.0	27	3	US-08-485-355B-4	Sequence 4, Appli
C 33	12	60.0	29	3	US-09-045-583-45	Sequence 45, Appl
C 34	12	60.0	29	3	US-09-534-185-45	Sequence 45, Appl
C 35	12	60.0	32	3	US-08-485-355B-30	Sequence 30, Appl
C 36	12	60.0	32	3	US-09-045-583-44	Sequence 44, Appl
C 37	12	60.0	32	3	US-09-534-185-44	Sequence 44, Appl
C 38	11.8	59.0	17	2	US-08-171-299B-6	Sequence 6, Appli
C 39	11.8	59.0	20	3	US-09-467-642-13	Sequence 13, Appl
C 40	11.8	59.0	23	3	US-08-930-797B-2	Sequence 2, Appli
C 41	11.8	59.0	27	2	US-08-580-401-5	Sequence 5, Appli
C 42	11.8	59.0	27	2	US-08-927-394-8	Sequence 8, Appli
C 43	11.8	59.0	31	2	US-08-927-394-7	Sequence 7, Appli
C 44	11.6	58.0	18	3	US-09-402-618B-75	Sequence 75, Appl
C 45	11.6	58.0	18	3	US-09-942-588A-31	Sequence 31, Appl

ALIGNMENTS

RESULT 1
US-09-977-137A-16
; Sequence 16, Application US/09977137A
; Patent No. 6750042
; GENERAL INFORMATION:
; APPLICANT: Summers, Anne O.
; APPLICANT: Caguat, Jonathan
; TITLE OF INVENTION: Metal Binding Proteins, Recombinant Host Cells and
; TITLE OF INVENTION: Methods
; FILE REFERENCE: 79-00
; CURRENT APPLICATION NUMBER: US/09/977,137A
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 60/240,465
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 33
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-09-977-137A-16

Qy	1	GGACCGCGGCTCGGTCA 19	Query Match 71.0%; Score 14.2; DB 3; Length 33;
Db	6	GGGTCTCGGCTCGGGCA 24	Best Local Similarity 84.2%; Pred. No. 3e+03; Mismatches 0; Indels 0; Gaps 0;
			Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

RESULT 2
US-09-396-196G-42173/c
; Sequence 42173, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678

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; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 42173
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-42173

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Best Local Similarity 100.0%; Pred. No. 3.8e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 CGGCGCTCGGTTCAT 20
Db 20 CGGCGCTCGGTTCAT 7

RESULT 3
US-09-396-196G-46323/c
; Sequence 46323, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396.196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 46323
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-46323

Query Match      69.0%; Score 13.8; DB 3; Length 25;
Best Local Similarity 88.2%; Pred. No. 4.6e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 ACGCGCGCTCGGTTCAT 20
Db 20 ACGCTGCGCACGGTTCAT 4

RESULT 4
US-09-396-196G-46324/c
; Sequence 46324, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396.196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 46324
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-46324

Query Match      69.0%; Score 13.8; DB 3; Length 25;
Best Local Similarity 88.2%; Pred. No. 4.6e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 ACGCGCGCTCGGTTCAT 20
Db 20 ACGCTGCGCACGGTTCAT 4

RESULT 5
US-09-396-196G-46335/c
; Sequence 46335, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396.196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 46335
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-46335

Query Match      69.0%; Score 13.8; DB 3; Length 25;
Best Local Similarity 88.2%; Pred. No. 4.6e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 ACGCGCGCTCGGTTCAT 20
Db 18 ACGCTGCGCACGGTTCAT 2

RESULT 6
US-09-396-196G-53301
; Sequence 53301, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396.196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 53301
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-53301

Query Match      66.0%; Score 13.2; DB 3; Length 25;
Best Local Similarity 83.3%; Pred. No. 8.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 GACGCGCGCTCGGTTCAT 20
Db 2 GACCCAGCGCTCTGTTCAT 19
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RESULT 7
US-09-046-858A-19
; Sequence 19, Application US/09046858A
; Patent No. 6048973
; GENERAL INFORMATION:
; APPLICANT: Rodriguez, Raymond L.
; TITLE OF INVENTION: SUGAR-REGULATORY SEQUENCES
; IN ALPHA-AMYLASE GENES
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: PO Box 60850
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/046,858A
; FILING DATE: 24-MAR-1998
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/042,376
; FILING DATE: 24-MAR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Dehlinger, Peter J.
; REGISTRATION NUMBER: 28,006
; REFERENCE/DOCKET NUMBER: 2000-0456.30
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-324-0880
; TELEFAX: 650-324-0960
; TELEX:
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-09-046-858A-19
Query Match 65.0%; Score 13; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GACGCGGCGCTCG 15
Db 2 GACGCGGCGCTCG 14

RESULT 9
US-10-206-654-19
; Sequence 19, Application US/10206654
; Patent No. 6919493
; GENERAL INFORMATION:
; APPLICANT: Rodriguez, Raymond L.
; TITLE OF INVENTION: SUGAR-REGULATORY SEQUENCES
; IN ALPHA-AMYLASE GENES
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: PO Box 60850
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/206,654
; FILING DATE: 25-Jul-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/046,858A
; FILING DATE: 24-MAR-1998
; APPLICATION NUMBER: 60/042,376
; FILING DATE: 24-MAR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Dehlinger, Peter J.
; REGISTRATION NUMBER: 28,006
; REFERENCE/DOCKET NUMBER: 2000-0456.30
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-324-0880
; TELEFAX: 650-324-0960
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-10-206-654-19
Query Match 65.0%; Score 13; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GACGCGGCGCTCG 15
Db 2 GACGCGGCGCTCG 14

RESULT 8
US-09-450-515-19
; Sequence 19, Application US/09450515
; Patent No. 6680425
; GENERAL INFORMATION:
; APPLICANT: Rodriguez, Raymond L.
; TITLE OF INVENTION: SUGAR-REGULATORY SEQUENCES
; IN ALPHA-AMYLASE GENES
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: PO Box 60850
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/450,515
; FILING DATE: 25-Jul-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/046,858A
; FILING DATE: 24-MAR-1998
; APPLICATION NUMBER: 60/042,376
; FILING DATE: 24-MAR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Dehlinger, Peter J.
; REGISTRATION NUMBER: 28,006
; REFERENCE/DOCKET NUMBER: 2000-0456.30
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-324-0880
; TELEFAX: 650-324-0960
; TELEX:
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-09-450-515-19
Query Match 65.0%; Score 13; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GACGCGGCGCTCG 15
Db 2 GACGCGGCGCTCG 14
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; PRIOR APPLICATION NUMBER: US 60/177,740
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 60/177,739
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
US-09-538-864-14

Query Match 63.0%; Score 12.6; DB 3; Length 24;
Best Local Similarity 78.9%; Pred. No. 1.5e+04;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 GGACGGCGCGCTCGGTCAAT 20
Db 19 GCACGAGCGCTCGGATAT 1

RESULT 14
US-10-091-841A-35/c
; Sequence 35, Application US/10091841A
; Patent No. 6833493
; GENERAL INFORMATION:
; APPLICANT: Cho, Myeong-Je
; APPLICANT: Gel Val, Gregorio
; APPLICANT: Calliau, Maxime
; APPLICANT: Lemaux, Peggy G.
; APPLICANT: Buchanan, Bob B.
; TITLE OF INVENTION: BARLEY GENE FOR THIOREDUXIN AND
; TITLE OF INVENTION: NADP-THIOREDUXIN REDUCTASE
; FILE REFERENCE: 416272001410
; CURRENT APPLICATION NUMBER: US/10/091.841A
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 09/540,014
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: US 60/127,198
; PRIOR FILING DATE: 1999-03-31
; PRIOR APPLICATION NUMBER: US 60/169,162
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: US 60/177,740
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 60/177,739
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 35
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-10-091-841A-35

Query Match 63.0%; Score 12.6; DB 3; Length 24;
Best Local Similarity 78.9%; Pred. No. 1.5e+04;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 GGACGGCGCGCTCGGTCAAT 20
Db 19 GCACGAGCGCTCGGATAT 1

RESULT 15
US-09-396-196G-40648/c
; Sequence 40648, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann

; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 40648
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-40648

Query Match 63.0%; Score 12.6; DB 3; Length 25;
Best Local Similarity 78.9%; Pred. No. 1.5e+04;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 GGACGGCGCGCTCGGTCAAT 20
Db 25 GCACGGCGCGATCGATCAT 7

Search completed: November 27, 2005, 06:32:29
Job time : 135 secs

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OM nucleic - nucleic search, using sw model

Run on: November 27, 2005, 04:55:14 ; Search time 798 Seconds
(without alignments)
207.253 Million cell updates/sec

Title: US-10-605-498-82

Perfect score: 20

Sequence: 1 gggacgcgcgcgtcgatcat 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 10664982

Minimum DB seq length: 12

Maximum DB seq length: 35

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA.Main.*

- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq.*
- 2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq.*
- 3: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq.*
- 4: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq.*
- 5: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq.*
- 6: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq.*
- 7: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq.*
- 8: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq.*
- 9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq.*
- 10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	20	100.0	20	7	US-10-605-498-82
2	20	100.0	21	7	US-10-605-498-81
3	19	95.0	19	7	US-10-605-498-90
4	16	80.0	21	7	US-10-605-498-3
5	15.2	76.0	25	7	US-10-719-956-135321
6	15	75.0	21	7	US-10-605-498-4
7	14.2	71.0	25	10	US-11-036-317-261850
8	14.2	71.0	25	10	US-11-036-317-269817
9	14.2	71.0	25	10	US-11-036-317-330516
10	14.2	71.0	25	10	US-11-036-317-332488
11	14.2	71.0	25	10	US-11-036-317-364465
12	14.2	71.0	25	10	US-11-036-317-406575
13	14.2	71.0	25	10	US-11-036-317-536426
14	14.2	71.0	25	10	US-11-036-317-536427
15	14.2	71.0	33	3	US-09-977-137A-16
16	14	70.0	25	5	US-10-215-112-7242
17	14	70.0	25	9	US-10-809-189-42173
18	13.8	69.0	25	9	US-10-809-189-46323
19	13.8	69.0	25	9	US-10-809-189-46324
20	13.8	69.0	25	9	US-10-809-189-46335
21	13.6	68.0	25	7	US-10-719-956-135322
22	13.6	68.0	25	7	US-10-719-956-198103
23	13.6	68.0	25	8	US-10-719-900-309243

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24 13.6 68.0 25 10 US-11-036-317-912027 Sequence 912027,
25 13.6 68.0 25 10 US-11-036-317-912041 Sequence 912041,
c 26 13.2 66.0 25 5 US-10-098-263B-3853 Sequence 3853, Ap
27 13.2 66.0 25 5 US-10-098-263B-65789 Sequence 65789, A
28 13.2 66.0 25 7 US-10-719-956-110491 Sequence 110491,
c 29 13.2 66.0 25 7 US-10-719-956-547822 Sequence 547822,
c 30 13.2 66.0 25 7 US-10-719-956-547823 Sequence 547823,
31 13.2 66.0 25 8 US-10-719-900-148603 Sequence 148603,
32 13.2 66.0 25 8 US-10-719-900-849503 Sequence 849503,
33 13.2 66.0 25 8 US-10-719-900-849504 Sequence 849504,
34 13.2 66.0 25 9 US-10-809-189-53301 Sequence 53301, A
35 13.2 66.0 25 10 US-11-036-317-321539 Sequence 321539,
36 13.2 66.0 25 10 US-11-036-317-787134 Sequence 787134,
c 37 13.2 66.0 25 10 US-11-060-756-166335 Sequence 166335,
c 38 13.2 66.0 25 10 US-11-060-756-166384 Sequence 166384,
c 39 13.2 66.0 25 10 US-11-060-756-229339 Sequence 229339,
c 40 13.2 66.0 25 10 US-11-060-756-229340 Sequence 229340,
41 13 65.0 20 5 US-10-206-654-19 Sequence 19, Appl
42 13 65.0 25 7 US-10-719-956-634447 Sequence 634447,
43 13 65.0 25 10 US-11-036-317-883329 Sequence 883329,
44 13 65.0 25 10 US-11-036-317-937963 Sequence 937963,
45 12.8 64.0 24 5 US-10-193-692-3 Sequence 3, Appli

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ALIGNMENTS

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RESULT 1
US-10-605-498-82
; Sequence 82, Application US/10605498
; Publication No. US20040127441A1
; GENERAL INFORMATION:
; APPLICANT: Gleave, Martin
; APPLICANT: Rocchi, Palma
; APPLICANT: Signaevsky, Maxim
; TITLE OF INVENTION: Compositions and Methods for Treatment of Prostate and Other
; TITLE OF INVENTION: Cancers
; FILE REFERENCE: UBC.P-031
; CURRENT APPLICATION NUMBER: US/10/605,498
; CURRENT FILING DATE: 2003-10-02
; PRIOR FILING DATE: 2003-10-02
; PRIOR APPLICATION NUMBER: US 60/415,859
; PRIOR FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: US 60/463,952
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 82
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-605-498-82

Query Match 100.0%; Score 20; DB 7; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGACGCGCGCTCGGTGTCAT 20
   |||||
Db 1 GGGACGCGCGCTCGGTGTCAT 20

RESULT 2
US-10-605-498-81
; Sequence 81, Application US/10605498
; Publication No. US20040127441A1
; GENERAL INFORMATION:
; APPLICANT: Gleave, Martin
; APPLICANT: Rocchi, Palma
; APPLICANT: Signaevsky, Maxim
; TITLE OF INVENTION: Compositions and Methods for Treatment of Prostate and Other
; TITLE OF INVENTION: Cancers
; FILE REFERENCE: UBC.P-031
; CURRENT APPLICATION NUMBER: US/10/605,498

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; CURRENT FILING DATE: 2003-10-02
; PRIOR APPLICATION NUMBER: US 60/415,859
; PRIOR FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: US 60/463,952
; PRIOR FILING DATE: 2003-04-18
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 81
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-605-498-81

Query Match 100.0%; Score 20; DB 7; Length 21;
Best Local Similarity 100.0%; Pred. No. 5.5; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0;

Qy 1 GGGACGGCGCTCGGTTCAT 20
Db 2 GGGACGGCGCTCGGTTCAT 21
|||||

RESULT 3

US-10-605-498-90/c
; Sequence 90, Application US/10605498
; Publication No. US20040127441A1
; GENERAL INFORMATION:
; APPLICANT: Gleave, Martin
; APPLICANT: Rocchi, Palma
; APPLICANT: Signaevsky, Maxim
; TITLE OF INVENTION: Compositions and Methods for Treatment of Prostate and Other
; FILE REFERENCE: UBC-P-031
; CURRENT APPLICATION NUMBER: US/10/605,498
; CURRENT FILING DATE: 2003-10-02
; PRIOR APPLICATION NUMBER: US 60/415,859
; PRIOR FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: US 60/463,952
; PRIOR FILING DATE: 2003-04-18
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 90
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-605-498-90

Query Match 95.0%; Score 19; DB 7; Length 19;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GGGACGGCGCTCGGTTCAT 20
Db 19 GGGACGGCGCTCGGTTCAT 1
|||||

RESULT 4

US-10-605-498-3
; Sequence 3, Application US/10605498
; Publication No. US20040127441A1
; GENERAL INFORMATION:
; APPLICANT: Gleave, Martin
; APPLICANT: Rocchi, Palma
; APPLICANT: Signaevsky, Maxim
; TITLE OF INVENTION: Compositions and Methods for Treatment of Prostate and Other
; FILE REFERENCE: UBC-P-031
; CURRENT APPLICATION NUMBER: US/10/605,498
; CURRENT FILING DATE: 2003-10-02
; PRIOR APPLICATION NUMBER: US 60/415,859
; PRIOR FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: US 60/463,952
; PRIOR FILING DATE: 2003-04-18

; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-605-498-3

Query Match 80.0%; Score 16; DB 7; Length 21;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 CGCGCGCTCGGTTCAT 20
Db 1 CGCGCGCTCGGTTCAT 16
|||||

RESULT 5

US-10-719-956-135321/c
; Sequence 135321, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 135321
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-135321

Query Match 76.0%; Score 15.2; DB 7; Length 25;
Best Local Similarity 85.0%; Pred. No. 1.2e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GGGACGGCGCTCGGTTCAT 20
Db 25 GGGACGAACGCTCGGCAT 6
|||||

RESULT 6

US-10-605-498-4
; Sequence 4, Application US/10605498
; Publication No. US20040127441A1
; GENERAL INFORMATION:
; APPLICANT: Gleave, Martin
; APPLICANT: Rocchi, Palma
; APPLICANT: Signaevsky, Maxim
; TITLE OF INVENTION: Compositions and Methods for Treatment of Prostate and Other
; FILE REFERENCE: UBC-P-031
; CURRENT APPLICATION NUMBER: US/10/605,498
; CURRENT FILING DATE: 2003-10-02
; PRIOR APPLICATION NUMBER: US 60/415,859
; PRIOR FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: US 60/463,952
; PRIOR FILING DATE: 2003-04-18
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-605-498-4

Query Match 75.0%; Score 15; DB 7; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;

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Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGACGGCGGCTCG 15
    |||||
Db 7 GGGACGGCGGCTCG 21

RESULT 7
US-11-036-317-261850
; Sequence 261850, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 261850
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-261850

Query Match 71.0%; Score 14.2; DB 10; Length 25;
Best Local Similarity 84.2%; Pred. No. 3.6e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GGGACGGCGGCTCGGTCA 19
    |||||
Db 3 GGGACGGCGGATCTGCCA 21

RESULT 8
US-11-036-317-269817
; Sequence 269817, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 269817
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-269817

Query Match 71.0%; Score 14.2; DB 10; Length 25;
Best Local Similarity 84.2%; Pred. No. 3.6e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GGGACGGCGGCTCGGTCA 19
    |||||
Db 5 GGGACGGCGGATCTGCCA 23

RESULT 9
US-11-036-317-330516
; Sequence 330516, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
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; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 330516
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-330516

Query Match 71.0%; Score 14.2; DB 10; Length 25;
Best Local Similarity 84.2%; Pred. No. 3.6e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GGGACGGCGGCTCGGTCA 19
    |||||
Db 1 GGGACGGCGGATCTGCCA 19

RESULT 10
US-11-036-317-332488
; Sequence 332488, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 332488
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-332488

Query Match 71.0%; Score 14.2; DB 10; Length 25;
Best Local Similarity 84.2%; Pred. No. 3.6e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GGGACGGCGGCTCGGTCA 19
    |||||
Db 2 GGGACGGCGGATCTGCCA 20

RESULT 11
US-11-036-317-364465
; Sequence 364465, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 364465
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
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US-11-036-317-364465

Query Match 71.0%; Score 14.2; DB 10; Length 25;
Best Local Similarity 84.2%; Pred. No. 3.6e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GGGACGCGGCGCTCGGTCA 19
||||| ||||| ||||| ||||| |||||
Db 4 GGGACGCGGCGATCTGCCA 22

RESULT 12

US-11-036-317-406575
; Sequence 406575, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036.317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 406575
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
; US-11-036-317-406575

Query Match 71.0%; Score 14.2; DB 10; Length 25;
Best Local Similarity 84.2%; Pred. No. 3.6e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GGGACGCGGCGCTCGGTCA 19
||||| ||||| ||||| ||||| |||||
Db 7 GGGACGAGGCGCTTTGTCA 25

RESULT 13

US-11-036-317-536426
; Sequence 536426, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036.317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 536426
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
; US-11-036-317-536426

Query Match 71.0%; Score 14.2; DB 10; Length 25;
Best Local Similarity 84.2%; Pred. No. 3.6e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GGGACGCGGCGCTCGGTCA 19
||||| ||||| ||||| ||||| |||||
Db 7 GGGACGAGGCGCTTTGTCA 25

RESULT 14

US-11-036-317-536427

; Sequence 536427, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036.317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 536427
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
; US-11-036-317-536427

Query Match 71.0%; Score 14.2; DB 10; Length 25;
Best Local Similarity 84.2%; Pred. No. 3.6e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GGGACGCGGCGCTCGGTCA 19
||||| ||||| ||||| ||||| |||||
Db 7 GGGACGTCGGGCTTTGTCA 25

RESULT 15

US-09-977-137A-16
; Sequence 16, Application US/09977137A
; Publication No. US20030104524A1
; GENERAL INFORMATION:
; APPLICANT: Summers, Anne O.
; APPLICANT: Caguiat, Jonathan
; TITLE OF INVENTION: Metal Binding Proteins, Recombinant Host Cells and
; TITLE OF INVENTION: Methods
; FILE REFERENCE: 79-00
; CURRENT APPLICATION NUMBER: US/09/977,137A
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 60/240,465
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 33
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
; US-09-977-137A-16

Query Match 71.0%; Score 14.2; DB 3; Length 33;
Best Local Similarity 84.2%; Pred. No. 3.4e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GGGACGCGGCGCTCGGTCA 19
||||| ||||| ||||| ||||| |||||
Db 6 GGGTCGCGGCGCTCGGGCA 24

Search completed: November 27, 2005, 06:46:02
Job time : 798 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 27, 2005, 04:57:00 ; Search time 225 Seconds
(without alignments)
13.210 Million cell updates/sec

Title: US-10-605-498-82

Perfect score: 20

Sequence: 1 gggacgcggcgctcggtcat 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3205263 seqs, 74304013 residues

Total number of hits satisfying chosen parameters: 6389384

Minimum DB seq length: 12

Maximum DB seq length: 35

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA.New.*
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2: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq.*
3: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq.*
4: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq.*
5: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq.*
6: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq.*
7: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq.*
8: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq2.*
9: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq3.*
10: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	12.8	64.0	19	8 US-11-101-244-1008030	Sequence 1008030,
C 2	12.8	64.0	19	9 US-11-083-784-1008030	Sequence 1008030,
C 3	12.6	63.0	19	8 US-11-101-244-899787	Sequence 899787,
C 4	12.6	63.0	19	9 US-11-083-784-899787	Sequence 899787,
C 5	12.2	61.0	22	7 US-11-176-795-58	Sequence 58, Appl
C 6	12.2	61.0	22	7 US-11-176-795-58	Sequence 877585,
C 7	12	60.0	19	8 US-11-101-244-877585	Sequence 877585,
C 8	12	60.0	19	9 US-11-083-784-877585	Sequence 367704,
C 9	11.8	59.0	19	8 US-11-101-244-367704	Sequence 367704,
C 10	11.8	59.0	19	8 US-11-101-244-367714	Sequence 367714,
C 11	11.8	59.0	19	8 US-11-101-244-385820	Sequence 385820,
C 12	11.8	59.0	19	8 US-11-101-244-475963	Sequence 475963,
C 13	11.8	59.0	19	8 US-11-101-244-1128971	Sequence 1128971,
C 14	11.8	59.0	19	8 US-11-101-244-1221629	Sequence 1221629,
C 15	11.8	59.0	19	9 US-11-083-784-367704	Sequence 367704,
C 16	11.8	59.0	19	9 US-11-083-784-367714	Sequence 367714,
C 17	11.8	59.0	19	9 US-11-083-784-385820	Sequence 385820,
C 18	11.8	59.0	19	9 US-11-083-784-475963	Sequence 475963,
C 19	11.8	59.0	19	9 US-11-083-784-1128971	Sequence 1128971,
C 20	11.8	59.0	19	9 US-11-083-784-1221629	Sequence 1221629,
C 21	11.6	58.0	19	8 US-11-101-244-992967	Sequence 992967,
C 22	11.6	58.0	19	8 US-11-101-244-1512341	Sequence 1512341,
C 23	11.6	58.0	19	8 US-11-101-244-1562938	Sequence 1562938,

ALIGNMENTS

RESULT 1
US-11-101-244-1008030/c
; Sequence 1008030, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Reynolds, Bevin
; APPLICANT: Leake, Devlin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1008030
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1008030

Query Match 64.0%; Score 12.8; DB 8; Length 19;
Best Local Similarity 87.5%; Pred. No. 1.4e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 GACGCGCGCTCGGTC 18
Db 17 GATGAGCGCTCGGTC 2

RESULT 2
US-11-083-784-1008030/c
; Sequence 1008030, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Khvorova, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devlin
; APPLICANT: Marshall, William

Sequence 992967,
Sequence 1512341,
Sequence 1562938,
Sequence 199478,
Sequence 199517,
Sequence 186259,
Sequence 1044567,
Sequence 1436226,
Sequence 199478,
Sequence 199517,
Sequence 199517,
Sequence 1044567,
Sequence 1436226,
Sequence 135381,
Sequence 159112,
Sequence 184578,
Sequence 405926,
Sequence 406019,
Sequence 638817,
Sequence 1220367,
Sequence 1220305,

; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1008030
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1008030

Query Match 64.0%; Score 12.8; DB 9; Length 19;
Best Local Similarity 87.5%; Pred. No. 1.4e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GACGCGCGCTCGGTC 18
||| ||||| |||||
Db 17 GATGAGCGCTCGGTC 2

RESULT 3
US-11-101-244-899787
; Sequence 899787, Application US/1101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmaco, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 899787
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-899787

Query Match 63.0%; Score 12.6; DB 8; Length 19;
Best Local Similarity 63.2%; Pred. No. 1.7e+03;
Matches 12; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 2 GGACGGCGCTCGGTCAT 20
||| ||||| |||||
Db 1 GGAACGGCGCGUGUUCAU 19

RESULT 4
US-11-083-784-899787
; Sequence 899787, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmaco, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin

; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 899787
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-899787

Query Match 63.0%; Score 12.6; DB 9; Length 19;
Best Local Similarity 63.2%; Pred. No. 1.7e+03;
Matches 12; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 2 GGACGGCGCTCGGTCAT 20
||| ||||| |||||
Db 1 GGAACGGCGCGUGUUCAU 19

RESULT 5
US-11-176-795-58/c
; Sequence 58, Application US/11176795
; Publication No. US20050255517A1
; GENERAL INFORMATION:
; APPLICANT: Gerdes, John C
; APPLICANT: Marmaro, Jeffrey M
; TITLE OF INVENTION: Method and Device for Multiplex Amplification System
; FILE REFERENCE: 1
; CURRENT APPLICATION NUMBER: US/11/176,795
; CURRENT FILING DATE: 2005-07-07
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 58
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Coliform Bacteria
US-11-176-795-58

Query Match 61.0%; Score 12.2; DB 7; Length 22;
Best Local Similarity 82.4%; Pred. No. 2.4e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GGACGGCGCTCGGTC 18
||| ||||| |||||
Db 19 GGATCGCGCTCGGTC 3

RESULT 6
US-11-176-795-62/c
; Sequence 62, Application US/11176795
; Publication No. US20050255517A1
; GENERAL INFORMATION:
; APPLICANT: Gerdes, John C
; APPLICANT: Marmaro, Jeffrey M
; TITLE OF INVENTION: Method and Device for Multiplex Amplification System
; FILE REFERENCE: 1
; CURRENT APPLICATION NUMBER: US/11/176,795
; CURRENT FILING DATE: 2005-07-07
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 62
; LENGTH: 22
; TYPE: DNA

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; ORGANISM: Coliform Bacteria
US-11-176-795-62

Query Match      61.0%; Score 12.2; DB 7; Length 22;
Best Local Similarity 82.4%; Pred. No. 2.4e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY  2 GGACGGCGCGCTCGGTC 18
    ||| ||||| |||||
Db   19 GGATGCGCGCTCGGTC  3

RESULT 7
US-11-101-244-877585/c
; Sequence 877585, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 877585
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-877585

Query Match      60.0%; Score 12; DB 8; Length 19;
Best Local Similarity 100.0%; Pred. No. 3e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  9 GCGCTCGGTCAT 20
    ||| ||||| |||||
Db   15 GCGCTCGGTCAT  4

RESULT 8
US-11-083-784-877585/c
; Sequence 877585, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 877585
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-877585/c

Query Match      59.0%; Score 11.8; DB 8; Length 19;
Best Local Similarity 86.7%; Pred. No. 3.6e+03;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY  4 ACACGGCGCTCGGTC 18
    ||| ||||| |||||
Db   16 ACACGGCGCTCGGTC  2

RESULT 9
US-11-101-244-367704/c
; Sequence 367704, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 367704
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-367704

Query Match      60.0%; Score 12.2; DB 7; Length 22;
Best Local Similarity 82.4%; Pred. No. 2.4e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY  2 GGACGGCGCGCTCGGTC 18
    ||| ||||| |||||
Db   19 GGATGCGCGCTCGGTC  3

RESULT 10
US-11-101-244-367714/c
; Sequence 367714, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 367714
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-367714

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; ORGANISM: Homo sapiens
US-11-101-244-367714

Query Match      59.0%; Score 11.8; DB 8; Length 19;
Best Local Similarity 86.7%; Pred. No. 3.6e+03;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      4  ACGCGGCGCTCGGTC 18
      ||| ||| ||| ||| |||
Db      15  ACACGGCGCTTGGTC 1

RESULT 11
US-11-101-244-385820/c
; Sequence 385820, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 385820
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-385820

Query Match      59.0%; Score 11.8; DB 8; Length 19;
Best Local Similarity 86.7%; Pred. No. 3.6e+03;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      3  GACGCGCGCTCGGT 17
      ||| ||| ||| ||| |||
Db      17  GAGGTGGCGCTCGGT 3

RESULT 12
US-11-101-244-475963
; Sequence 475963, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 475963
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-475963

Query Match      59.0%; Score 11.8; DB 8; Length 19;
Best Local Similarity 86.7%; Pred. No. 3.6e+03;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      4  ACGCGGCGCTCGGTC 18
      ||| ||| ||| ||| |||
Db      17  ACACGGCGCTTGGTC 1

US-11-101-244-475963
; Sequence 1128971, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1128971
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1128971

Query Match      59.0%; Score 11.8; DB 8; Length 19;
Best Local Similarity 86.7%; Pred. No. 3.6e+03;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      4  ACGCGGCGCTCGGTC 18
      ||| ||| ||| ||| |||
Db      17  ACACGGCGCTTGGTC 3

RESULT 13
US-11-101-244-1221629/c
; Sequence 1221629, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1221629
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1221629
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Query Match 59.0%; Score 11.8; DB 8; Length 19;
Best Local Similarity 86.7%; Pred. No. 3.6e+03;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 ACGCGGCGCTCGGTC 18
||| | ||| ||| |||
Db 16 ACGTGAGCTCGGTC 2

RESULT 15
US-11-083-784-367704/c
; Sequence 367704, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 1349US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 367704
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-367704

Query Match 59.0%; Score 11.8; DB 9; Length 19;
Best Local Similarity 86.7%; Pred. No. 3.6e+03;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 ACGCGGCGCTCGGTC 18
||| | ||| ||| |||
Db 16 ACACGGCGCTTGTC 2

Search completed: November 27, 2005, 06:50:00
Job time : 226 secs

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